

SEQUENCE LISTING

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National Research Council of Canada

<120> Lipopolysaccharide alpha-2,3 Sialyltransferase of
Campylobacter jejuni and Its Uses

<130> 014137-013210US

<140> US 09/272,960
<141> 1999-03-18

<150> US 60/078,891
<151> 1998-03-20

<150> US 09/272,960
<151> 1999-03-18

<160> 7

<170> PatentIn Ver. 2.0

<210> 1
<211> 1293
<212> DNA
<213> Campylobacter jejuni

<220>
<221> CDS
<222> (1)..(1293)
<223> Campylobacter jejuni OH4384 cst-I gene
alpha2,3-sialyltransferase

<400> 1

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1				5					10					15		
caa	aat	ata	atc	ata	gca	gga	aat	gga	cct	agc	cta	aaa	aat	att	aat	96
Gln	Asn	Ile	Ile	Ile	Ala	Gly	Asn	Gly	Pro	Ser	Leu	Lys	Asn	Ile	Asn	
		20					25						30			
tat	aaa	aga	ctg	cct	aga	gaa	tat	gat	gtt	ttt	agg	tgt	aac	cag	ttt	144
Tyr	Lys	Arg	Leu	Pro	Arg	Glu	Tyr	Asp	Val	Phe	Arg	Cys	Asn	Gln	Phe	
		35					40					45				
tat	ttt	gaa	gat	aag	tat	tat	tta	gga	aaa	aag	att	aaa	gca	gta	ttt	192
Tyr	Phe	Glu	Asp	Lys	Tyr	Tyr	Leu	Gly	Lys	Lys	Ile	Lys	Ala	Val	Phe	
	50					55				60						
ttt	aat	cct	ggt	gtc	ttt	tta	caa	cag	tat	cac	act	gca	aaa	caa	ctt	240
Phe	Asn	Pro	Gly	Val	Phe	Leu	Gln	Gln	Tyr	His	Thr	Ala	Lys	Gln	Leu	
65					70				75					80		
ata	cta	aaa	aat	gag	tat	gaa	ata	aaa	aat	att	ttt	tgc	tct	aca	ttt	288
Ile	Leu	Lys	Asn	Glu	Tyr	Glu	Ile	Lys	Asn	Ile	Phe	Cys	Ser	Thr	Phe	
				85				90						95		

aat tta cct ttt att gaa agc aat gat ttt tta cat caa ttt tat aat	336
Asn Leu Pro Phe Ile Glu Ser Asn Asp Phe Leu His Gln Phe Tyr Asn	
100 105 110	
ttt ttc ccc gat gca aaa ctt ggc tat gaa gtt att gaa aac ctt aaa	384
Phe Phe Pro Asp Ala Lys Leu Gly Tyr Glu Val Ile Glu Asn Leu Lys	
115 120 125	
gaa ttt tat gct tat ata aaa tac aat gaa att tat ttc aat aaa aga	432
Glu Phe Tyr Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr Phe Asn Lys Arg	
130 135 140	
att act tcg ggc gtc tat atg tgt gca att gct att gca tta gga tat	480
Ile Thr Ser Gly Val Tyr Met Cys Ala Ile Ala Ile Ala Leu Gly Tyr	
145 150 155 160	
aaa acc atc tat tta tgt ggc att gat ttt tat gaa gga gat gtt att	528
Lys Thr Ile Tyr Leu Cys Gly Ile Asp Phe Tyr Glu Gly Asp Val Ile	
165 170 175	
tat cct ttt gaa gct atg agt aca aat ata aaa aca atc ttt cct gga	576
Tyr Pro Phe Glu Ala Met Ser Thr Asn Ile Lys Thr Ile Phe Pro Gly	
180 185 190	
ata aaa gat ttc aaa cct tca aat tgt cat tct aag gaa tac gat ata	624
Ile Lys Asp Phe Lys Pro Ser Asn Cys His Ser Lys Glu Tyr Asp Ile	
195 200 205	
gaa gca tta aaa ttg tta aaa tca ata tac aaa gtt aat atc tac gca	672
Glu Ala Leu Lys Leu Leu Lys Ser Ile Tyr Lys Val Asn Ile Tyr Ala	
210 215 220	
ttg tgt gat gat tct att ttg gca aat cat ttt cct tta tca att aat	720
Leu Cys Asp Asp Ser Ile Leu Ala Asn His Phe Pro Leu Ser Ile Asn	
225 230 235 240	
att aat aac aat ttc act tta gaa aat aag cat aat aat tct ata aat	768
Ile Asn Asn Asn Phe Thr Leu Glu Asn Lys His Asn Asn Ser Ile Asn	
245 250 255	
gat att tta ttg act gat aat act cct ggc gta agt ttt tat aaa aat	816
Asp Ile Leu Leu Thr Asp Asn Thr Pro Gly Val Ser Phe Tyr Lys Asn	
260 265 270	
caa ctt aaa gct gat aat aaa att atg ctt aat ttt tat aat att ctt	864
Gln Leu Lys Ala Asp Asn Lys Ile Met Leu Asn Phe Tyr Asn Ile Leu	
275 280 285	
cat tct aaa gat aat tta att aaa ttt tta aac aaa gaa att gcg gta	912
His Ser Lys Asp Asn Leu Ile Lys Phe Leu Asn Lys Glu Ile Ala Val	
290 295 300	
tta aaa aaa caa acc act caa cga gct aaa gca aga atc caa aac cat	960
Leu Lys Lys Gln Thr Thr Gln Arg Ala Lys Ala Arg Ile Gln Asn His	
305 310 315 320	
cta tcc tat aaa cta gga caa gct ttg att ata aat tct aaa agt gta	1008
Leu Ser Tyr Lys Leu Gly Gln Ala Leu Ile Ile Asn Ser Lys Ser Val	
325 330 335	

tta ggt ttt tta tct tta cct ttt ata ata tta agt atc gtt att tca 1056
 Leu Gly Phe Leu Ser Leu Pro Phe Ile Ile Leu Ser Ile Val Ile Ser
 340 345 350

cat aaa caa gaa caa aag gct tat aaa ttt aaa gta aag aaa aat cca 1104
 His Lys Gln Glu Gln Lys Ala Tyr Lys Phe Lys Val Lys Lys Asn Pro
 355 360 365

aat tta gct tta cct cct tta gaa act tat cct gat tat aat gaa gct 1152
 Asn Leu Ala Leu Pro Pro Leu Glu Thr Tyr Pro Asp Tyr Asn Glu Ala
 370 375 380

tta aaa gaa aaa gaa tgt ttt act tat aaa tta gga gaa gaa ttt ata 1200
 Leu Lys Glu Lys Glu Cys Phe Thr Tyr Lys Leu Gly Glu Glu Phe Ile
 385 390 395 400

aaa gct ggt aag aat tgg tat ggg gag ggg tat atc aaa ttt ata ttc 1248
 Lys Ala Gly Lys Asn Trp Tyr Gly Glu Gly Tyr Ile Lys Phe Ile Phe
 405 410 415

aaa gat gtt cct agg ttg aag aga gag ttt gag aaa ggg gaa taa 1293
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 420 425 430

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 <212> PRT
 <213> Campylobacter jejuni

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Gln Asn Ile Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Asn Ile Asn
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Tyr Lys Arg Leu Pro Arg Glu Tyr Asp Val Phe Arg Cys Asn Gln Phe
 35 40 45

Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Ile Lys Ala Val Phe
 50 55 60

Phe Asn Pro Gly Val Phe Leu Gln Gln Tyr His Thr Ala Lys Gln Leu
 65 70 75 80

Ile Leu Lys Asn Glu Tyr Glu Ile Lys Asn Ile Phe Cys Ser Thr Phe
 85 90 95

Asn Leu Pro Phe Ile Glu Ser Asn Asp Phe Leu His Gln Phe Tyr Asn
 100 105 110

Phe Phe Pro Asp Ala Lys Leu Gly Tyr Glu Val Ile Glu Asn Leu Lys
 115 120 125

Glu Phe Tyr Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr Phe Asn Lys Arg
 130 135 140

Ile Thr Ser Gly Val Tyr Met Cys Ala Ile Ala Ile Ala Leu Gly Tyr
 145 150 155 160

Lys Thr Ile Tyr Leu Cys Gly Ile Asp Phe Tyr Glu Gly Asp Val Ile
 165 170 175
 Tyr Pro Phe Glu Ala Met Ser Thr Asn Ile Lys Thr Ile Phe Pro Gly
 180 185 190
 Ile Lys Asp Phe Lys Pro Ser Asn Cys His Ser Lys Glu Tyr Asp Ile
 195 200 205
 Glu Ala Leu Lys Leu Leu Lys Ser Ile Tyr Lys Val Asn Ile Tyr Ala
 210 215 220
 Leu Cys Asp Asp Ser Ile Leu Ala Asn His Phe Pro Leu Ser Ile Asn
 225 230 235 240
 Ile Asn Asn Asn Phe Thr Leu Glu Asn Lys His Asn Asn Ser Ile Asn
 245 250 255
 Asp Ile Leu Leu Thr Asp Asn Thr Pro Gly Val Ser Phe Tyr Lys Asn
 260 265 270
 Gln Leu Lys Ala Asp Asn Lys Ile Met Leu Asn Phe Tyr Asn Ile Leu
 275 280 285
 His Ser Lys Asp Asn Leu Ile Lys Phe Leu Asn Lys Glu Ile Ala Val
 290 295 300
 Leu Lys Lys Gln Thr Thr Gln Arg Ala Lys Ala Arg Ile Gln Asn His
 305 310 315 320
 Leu Ser Tyr Lys Leu Gly Gln Ala Leu Ile Ile Asn Ser Lys Ser Val
 325 330 335
 Leu Gly Phe Leu Ser Leu Pro Phe Ile Ile Leu Ser Ile Val Ile Ser
 340 345 350
 His Lys Gln Glu Gln Lys Ala Tyr Lys Phe Lys Val Lys Lys Asn Pro
 355 360 365
 Asn Leu Ala Leu Pro Pro Leu Glu Thr Tyr Pro Asp Tyr Asn Glu Ala
 370 375 380
 Leu Lys Glu Lys Glu Cys Phe Thr Tyr Lys Leu Gly Glu Glu Phe Ile
 385 390 395 400
 Lys Ala Gly Lys Asn Trp Tyr Gly Glu Gly Tyr Ile Lys Phe Ile Phe
 405 410 415
 Lys Asp Val Pro Arg Leu Lys Arg Glu Phe Glu Lys Gly Glu
 420 425 430

<210> 3

<211> 41

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:CJ18F 5' primer

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41

<210> 4
 <211> 60
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence:CJ40R 3' primer

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<210> 5
 <211> 231
 <212> PRT
 <213> Haemophilus influenzae

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 <223> Haemophilus influenzae Rd putative open reading
 frame (ORF)

<400> 5
 Met Gln Leu Ile Lys Asn Asn Glu Tyr Glu Tyr Ala Asp Ile Ile Leu
 1 5 10 15
 Ser Ser Phe Val Asn Leu Gly Asp Ser Glu Leu Lys Lys Ile Lys Asn
 20 25 30
 Val Gln Lys Leu Leu Thr Gln Val Asp Ile Gly His Tyr Tyr Leu Asn
 35 40 45
 Lys Leu Pro Ala Phe Asp Ala Tyr Leu Gln Tyr Asn Glu Leu Tyr Glu
 50 55 60
 Asn Lys Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Thr Val
 65 70 75 80
 Met Gly Tyr Lys Asp Leu Tyr Leu Thr Gly Ile Asp Phe Tyr Gln Glu
 85 90 95
 Lys Gly Asn Pro Tyr Ala Phe His His Gln Lys Glu Asn Ile Ile Lys
 100 105 110
 Leu Leu Pro Ser Phe Ser Gln Asn Lys Ser Gln Ser Asp Ile His Ser
 115 120 125
 Met Glu Tyr Asp Leu Asn Ala Leu Tyr Phe Leu Gln Lys His Tyr Gly
 130 135 140
 Val Asn Ile Tyr Cys Ile Ser Pro Glu Ser Pro Leu Cys Asn Tyr Phe
 145 150 155 160
 Pro Leu Ser Pro Leu Asn Asn Pro Ile Thr Phe Ile Leu Glu Glu Lys
 165 170 175
 Lys Asn Tyr Thr Gln Asp Ile Leu Ile Pro Pro Lys Phe Val Tyr Lys
 180 185 190

Lys Ile Gly Ile Tyr Ser Lys Pro Arg Ile Tyr Gln Asn Leu Ile Phe
 195 200 205

Arg Leu Ile Trp Asp Ile Leu Arg Leu Pro Asn Asp Ile Lys His Ala
 210 215 220

Leu Lys Ser Arg Lys Trp Asp
 225 230

<210> 6

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:6 His tail
 (His)6

<400> 6

His His His His His His
 1 5

<210> 7

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:linker between
 two fusion protein domains

<400> 7

Gly Gly Gly His
 1